

Figure 1

1 CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC CTGGTCACAG TGAGCCGTTT
 61 GCCCCCGGGC AGCGGCGCCT CCACGCCCGT GGGGCCCTGG GACCAGGCGG TCCAGCGAAG
 121 GAGTCGACTC CAGCGAAGGC AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA
 181 GGATGGAGGG GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC
 241 GAGTGAGGAG GAGCTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC AGAGTCCCCA
 301 GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA CAGCTGCTGA GGCCGAGGA
 361 TGACATCCGC CTGGCAGCCC AGCTGGAGGC ACCCGGCCCT CCCC GGCTCC GCTACCTGCT
 421 GGTAGTTTCT ACACGAGAAG GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT
 481 GGATTTCCCT GACAGCAGCT CCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG
 541 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG GTGGGCAAAG
 601 CCGGATCTTC AAGCCCCTCT CCATCCAGAC CATGTGGGCC AACTCCAGG TATTGCACCA
 661 AGCATGTGAG GCAGCTCTAG GCAGCGGCCT TGTACCGGGT GGCAGTGCCC TCACCTGGGC
 721 CAGCCACTAC CAGGAGAGAC TGAATCCGA ACAGAGCTGC CTCAATGAGT GGACGGCTAT
 781 GGCCGACCTG GAGTCTCTGC GGCCTCCCAG CGCCGAGCCT GGCGGGTCTT CAGAACAGGA
 841 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA GTGACCTGGA
 901 GAGTGTCAT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG CGCCTGGGGC TCCCCCTCCA
 961 GCAGTACCGT GACTTCATCG ACAACCAGAT GCTGCTGCTG GTGGCACAGC GGGACCGAGC
 1021 CTCCCGCATC TTCCCCCACC TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA
 1081 GCTGCAGAGG AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA
 1141 CCCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG CCCAGCTGCT
 1201 GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA AGAGCACAGG GCACCCACGT
 1261 GCTGGTCCAC TGCAAGATGG GCGTCAGCCG CTCAGCGGCC ACAGTGCTGG CCTATGCCAT
 1321 GAAGCAGTAC GAATGCAGCC TGGAGCAGGC CCTGCGCCAC GTGCAGGAGC TCCGGCCCAT
 1381 CGCCCGCCCC AACCTTGCTC TCCTGCGCCA GCTGCAGATC TACCAGGGCA TCCTGACGGC
 1441 CAGCCGCCAG AGCCATGTCT GGGAGCAGAA AGTGGGTGGG GTCTCCCCAG AGGAGCACCC
 1501 AGCCCTTGAA GTCTCTACAC CATTCACCACC TCTTCCGCCA GAACCTGAGG GTGGTGGGGA
 1561 GGAGAAGGTT GTAGGCATGG AAGAGAGCCA GGCAGCCCCG AAAGAAGAGC CTGGGCCACG
 1621 GCCACGTATA AACCTCCGAG GGGTCATGAG GTCCATCAGT CTTCTGGAGC CCTCCTTGGA
 1681 GCTGGAGAGC ACCTCAGAGA CCAAGTACAT GCCAGAGGTC TTCTCTTCCC ACGAGTCTTC
 1741 ACATGAAGAG CCTCTGCAGC CCTTCCCACA GCTTGCAAGG ACCAAGGGAG GCCAGCAGGT
 1801 GGACAGGGGG CCTCAGCCTG CCCTGAAGTC CCGCCAGTCA GTGGTTACCC TCCAGGGCAG
 1861 TGCCGTGGTG GCCAACCAGA CCCAGGCCTT CCAGGAGCAG GAGCAGGGGC AGGGGCAGGG
 1921 GCAGGGAGAG CCCTGCATTT CCTCTACGCG CAGGTTCCGG AAGGTGGTGA GACAGGCCAG
 1981 CGTGCATGAC AGTGAGAGAG AGGGCGAGGC CTGAGCCCTC ACACATGCCC ACGTCCCCCT
 2041 GACACTGAAG AGGATCCACA ACTCCTTGGA GAAACACCCT CACGTCTGTT GCCGCACACA
 2101 TTCCTCTCAG CTCCGCCCCA TACCCGTCAC TACAGCCTCA CCTCCCACCC CTGTCACTAC
 2161 GGCTCACCT CCCACCCCTG TCACTACAGC CTCACCTCCT ACAGCCTTAA GTCCCAGGCC
 2221 CATGTCTGCC TGTCCAAGGG CTCAAGACTT TCTAACTGGG ATGTGGTAGA GGGACTGAAG
 2281 GTACCTTTGG GGGCAACAGC ACCCTAGTTT CATTCTCAAC TCTAGCCCTG CACTCACC
 2341 TGTGGCACGG AATGAAAACA GAGCTTCCCG TGCAAAAAGG GTCACGCCTC CCACCCCGC
 2401 CCCCTCCCTG CACCTCCTGT CCTCTCCCAG TTCATTCTG GAACCAGCCA GGCCAGGCAA
 2461 CCAAGTGGCC CCAAAGGCAG GCAGGATCCT CAGGCCCCAG CCGCGGGAGG CTGGAAGGGC
 2521 TGGCAGATCG CTTCCCTCAT CCACCTCCAC CGGTCCAGGT CTTTGCTGCT GTCCCCAGAC
 2581 CTCCTGTGAC ACCACGCCAG ATCACAGGGC ACCAGGCCAG AGATAGTCTT CTTTTGTCC
 2641 TTTCTGGCCT CTGGCTAGTC AGTTTTTCAT AGCCTTACAG TATCTGGCTT TGTACTGAGA
 2701 AATAAAACAC ATTTTCAT

MALVTVSRSPPGSGASTPVPGWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEASSEPTKAPSEELHGD
QTDFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAPRPRLRYLLVVSTREGEGLSQDETVLLGVDFPDS
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YQERLNSEQSCLNEWTAMADLESRLPPSAEPGGSSEQEQQEQAIRAEWLKVLVDSDLESVTSKEIRQALELRGLPL
QQYRDFIDNQMLLLVAQRDRASRIFPHLYLGSEWNAANLEELQRNRVTHILNMAREIDNFYPERFITYHNVRWDEES
AQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRSAATVLAYAMKQYECSSLEQALRHVQELRPIARPNPGLRQLQI
YQGILTASRQSHVWEQKVGGVSPEEHPAPEVSTPFPPLPPEPEGGGEEKVVGMEESQAAPKEEPPRPRINLRGVMR
SISLLEPSLELESTSETSDMPEVFSSHESSHEEPLQPFQPLARTKGGQQVDRGPQPAKLSRQSVVTLQGSVVANRT
QAFQEQEQQGGQGGQGEPCISSTPRFRKVVVRQASVHDSGEEGEA

[illegible][illegible]

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91 100 110 120 130 140 150 160 164
|-----+-----+-----+-----+-----+-----+-----+-----+
FIDEA-RGKNCGVLVHCLAGISRSVTVVAYLMQKHL SHNDAYDVIYKHKKSNI SPNFNFGQLLOFERTLGLS
FIDEA-RSKKCGVLVHCLAGISRSVTVVAYLMQKMNLSLNDAYDFVYKHKKSNI SPNFNFGQLLOFERTLGLS
FIDEA-LSQNCGVLVHCLAGISRSVTVVAYLMQKHL SLNDAYDLVYKHKKSNI SPNFNFGQLLOFERSLRLE
FIDKA-KLSSCQVIVHCLAGISRSATIAIAYIMKTHGMSDDAYRFVYKDRRPSISPNFNFLGQLLEYERTLKL
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FIEAA-RAQGTHTVLVHCKMGVSRSAATVLAAYAMKQYECSEQLRHYQELRPIARPMPGFLRQLQIYQGIL TAR
FI#.a.....VIVHC.aGiRSat....AYLM.....sl..R....ik..r...isPnf.F$gQLl..#.l....

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Figure 4

1 CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC CTGGTCACAG TGAGCCGTTT
61 GCCCCCGGGC AGCGGCGCCT CCACGCCCCT GGGGCCCTGG GACCAGGCGG TCCAGCGAAG
121 GAGTCGACTC CAGCGAAGGC AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA
181 GGATGGAGGG GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC
241 GAGTGAGGAG GAGCTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC AGAGTCCCCA
301 GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA CAGCTGCTGA GGCCGCAGGA
361 TGACATCCGC CTGGCAGCCC AGCTGGAGGC ACCCGGCCT CCCC GGCTCC GCTACCTGCT
421 GGTA GTTTCT ACACGAGAAG GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT
481 GGATTTCCCT GACAGCAGCT CCCCCAGCTG CACCTGGGC CTGGTCTTGC CCCTCTGGAG
541 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG GTGGGCAAAG
601 CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGTGGGCC AACTCCAGG TATTGCACCA
661 AGCATGTGAG GCAGCTCTAG GCAGCGGCCT TGTACGGGT GGCAGTGCCC TCACCTGGGC
721 CAGCCACTAC CAGGAGAGAC TGAATCCGA ACAGAGCTGC CTCAATGAGT GGACGGCTAT
781 GGCCGACCTG GAGTCTCTGC GGCCTCCAG CGCCGAGCCT GCGGGTCTT CAGAACAGGA
841 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA GTGACCTGGA
901 GAGTGTCACT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG CGCCTGGGGC TCCCCCTCCA
961 GCAGTACCGT GACTTCATCG ACAACCAGAT GCTGCTGCTG GTGGCACAGC GGGACCGAGC
1021 CTCCCGCATC TTCCCCACC TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA
1081 GCTGCAGAGG AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA
1141 CCCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG CCCAGCTGCT
1201 GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA AGAGCACAGG GCACCCACGT
1261 GCTGGTCCAC TGCAAGATGG GCGTCAGCCG CTCAGCGGCC ACAGTGCTGG CCTATGCCAT
1321 GAAGCAGTAC GAATGCAGCC TGGAGCAGGC CCTGCGCCAC GTGCAGGAGC TCCGGCCCAT
1381 CGCCCGCCCC AACCCTGGCT TCCTGCGCCA GTGTCAGATC TACCAGGGCA TCCTGACGGC
1441 CAGAACCTGA GGGTGGTGGG GAGGAGAAGG TTGTAGGCAT GGAAGAGAGC CAGGCAGCCC
1501 CGAAAGAAGA GCCTGGGCCA CGGCCACGTA TAAACCTCCG AGGGGTCATG AGGTCCATCA
1561 GTCTTCTGGA GCCCTCCTTG GAGCTGGAGA GCACCTCAGA GACCAGTGAC ATGCCAGAGG
1621 TCTTCTCTTC CCACGAGTCT TCACATGAAG AGCCTCTGCA GCCCTTCCCA CAGCTTGCAA
1681 GGACCAAGGG AGGCCAGCAG GTGGACAGGG GGCCTCAGCC TGCCCTGAAG TCCCGCCAGT
1741 CAGTGGTTAC CCTCCAGGGC AGTGCCGTGG TGGCCAACCG GACCCAGGCC TTCCAGGAGC
1801 AGGAGCAGGG GCAGGGGCAG GGGCAGGGAG AGCCCTGCAT TTCCTCTACG CCCAGGTTCC
1861 GGAAGGTGGT GAGACAGGCC AGCGTGCATG ACAGTGGAGA GGAGGGCGAG GCCTGAGCCC
1921 TCACACATGC CCACGCTCCC CTGACACTGA AGAGGATCCA CAACTCCTTG GAGAAACACC
1981 CTCACGTCTG TTGCCGCACA CATTCCTCTC AGCTCCGCCC CATACCCGTC ACTACAGCCT
2041 CACCTCCCAC CCCTGTCACT ACGGCCTCAC CTCCCACCCC GTCACTACA GCCTCACCTC
2101 CTACAGCCTT AAGTCCCAGG CCCATGTCTG CCTGTCCAAG GGCTCAAGAC TTTCTAACTG
2161 GGATGTGGTA GAGGGACTGA AGGTACCTTT GGGGGCAACA GCACCTAGT TTCATTCTCA
2221 ACTCTAGCCC TGCACTACTCA CCTGTGGCAC GGAATGAAAA CAGAGCTTCC CGTGCAAAAA
2281 GGGTCACGCC TCCCACCCCC GCCCCCTCCC TGCACCTCCT GTCCTCTCCC AGTTCACTCC
2341 TGGAAACCAGC CAGGCCAGGC AACCAGTGGC CCCCAAAGGC AGGCAGGATC CTCAGGCCCC
2401 AGCCGCGGGA GGCTGGAAGG GCTGGCAGAT CGTTCCCTC ATCCACCTCC ACCGGTCCAG
2461 GTCTTTGCTG CTGTCCCCAG ACCTCCTGTG ACACCACGCC AGATCACAGG GCACCAGGCC
2521 AGAGATAGTC TTCTTTTTGT CCTTTCTGGC CTCTGGCTAG TCAGTTTTTC ATAGCCTTAC
2581 AGTATCTGGC TTTGTACTGA GAAATAAAAC ACATTTTC

Figure 5

MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFVLRGAVLGLQDGGDNDAAEASSEPTKAPSEEEELHGD
QTDFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAPRPRLRYLLVVSTREGEGLSQDETIVLLGVDFPDS
SSPCTLGLVPLWSDTQVYLDGGGFSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASH
YQERLNSEQSCLNEWTAMADLES LRPPSAEPGGSSEQEQMEQAI RAE LWKVL DVSDLESVTSKEIRQALELRGLPL
QQYRDFIDNQMLLLVAQRDRASRIFPHLYLGSEWNAANLEELQRNRVTHILNMAREIDNFYPERFTYHNVRLWDEES
AQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRSAATV LAYAMKQYEC SLEQALRHVQELRPIARPNPGFLRQLQI
YQGILTART

2004-0433

DSP-15	1	10	20	30	40	50	60	70	80	90	100	110	120	130
AB036834	1	10	20	30	40	50	60	70	80	90	100	110	120	130
DSP-13	1	10	20	30	40	50	60	70	80	90	100	110	120	130
DSP-12	1	10	20	30	40	50	60	70	80	90	100	110	120	130
Consensus	1	10	20	30	40	50	60	70	80	90	100	110	120	130
DSP-15	131	140	150	160	170	180	190	200	210	220	230	240	250	260
AB036834	131	140	150	160	170	180	190	200	210	220	230	240	250	260
DSP-13	131	140	150	160	170	180	190	200	210	220	230	240	250	260
DSP-12	131	140	150	160	170	180	190	200	210	220	230	240	250	260
Consensus	131	140	150	160	170	180	190	200	210	220	230	240	250	260
DSP-15	261	270	280	290	300	310	320	330	340	350	360	370	380	390
AB036834	261	270	280	290	300	310	320	330	340	350	360	370	380	390
DSP-13	261	270	280	290	300	310	320	330	340	350	360	370	380	390
DSP-12	261	270	280	290	300	310	320	330	340	350	360	370	380	390
Consensus	261	270	280	290	300	310	320	330	340	350	360	370	380	390
DSP-15	391	400	410	420	430	440	450	460	470	480	490	500	510	520
AB036834	391	400	410	420	430	440	450	460	470	480	490	500	510	520
DSP-13	391	400	410	420	430	440	450	460	470	480	490	500	510	520
DSP-12	391	400	410	420	430	440	450	460	470	480	490	500	510	520
Consensus	391	400	410	420	430	440	450	460	470	480	490	500	510	520
DSP-15	521	530	540	550	560	570	580	590	600	610	620	630	640	650
AB036834	521	530	540	550	560	570	580	590	600	610	620	630	640	650
DSP-13	521	530	540	550	560	570	580	590	600	610	620	630	640	650
DSP-12	521	530	540	550	560	570	580	590	600	610	620	630	640	650
Consensus	521	530	540	550	560	570	580	590	600	610	620	630	640	650
DSP-15	651	660	670	680	690	700	710	720	730	740	750	760	770	780
AB036834	651	660	670	680	690	700	710	720	730	740	750	760	770	780
DSP-13	651	660	670	680	690	700	710	720	730	740	750	760	770	780
DSP-12	651	660	670	680	690	700	710	720	730	740	750	760	770	780
Consensus	651	660	670	680	690	700	710	720	730	740	750	760	770	780